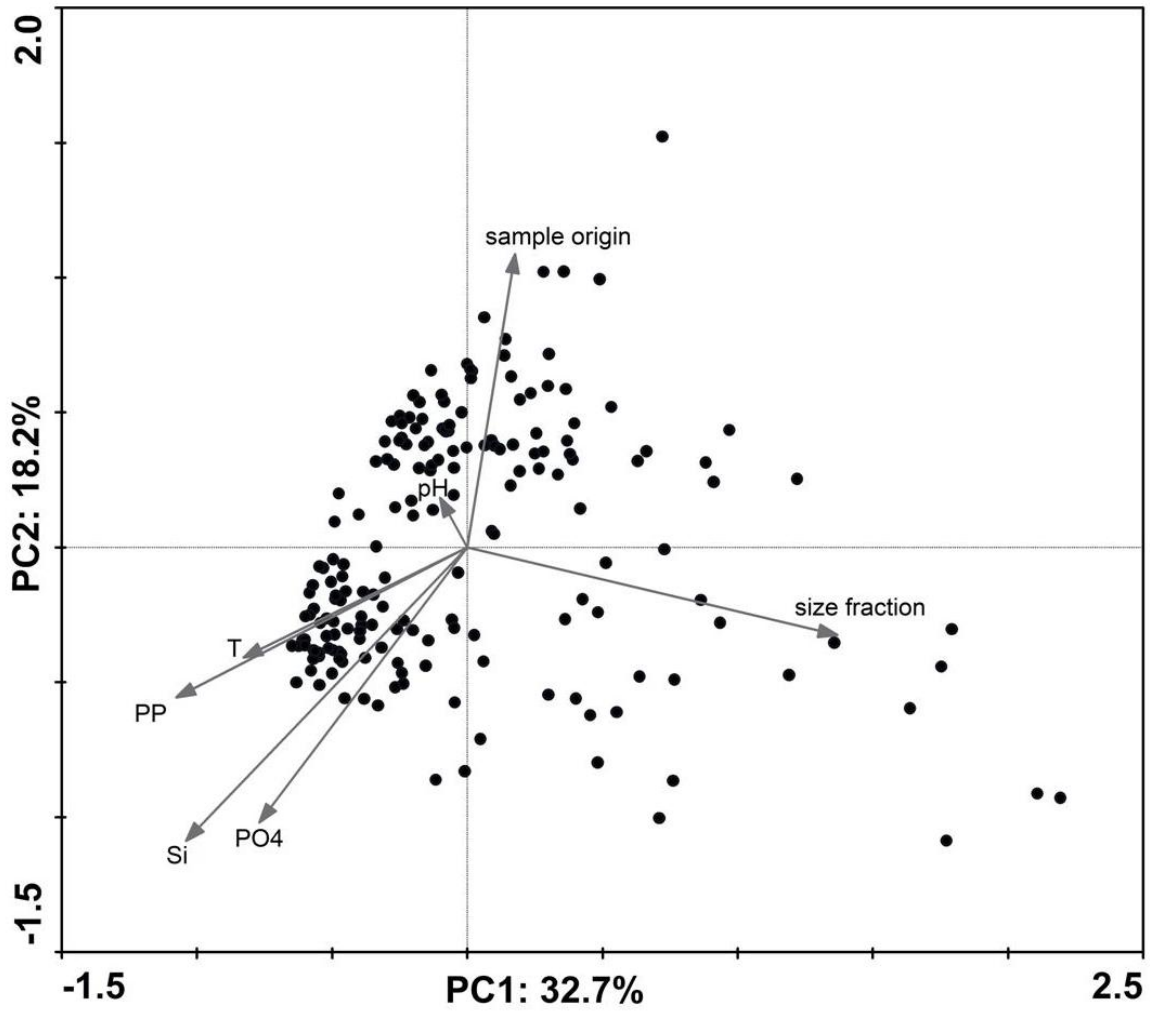

Fig. S1. Principal coordinates analysis (PCoA) with significant environmental variables overlaid as supplementary data.

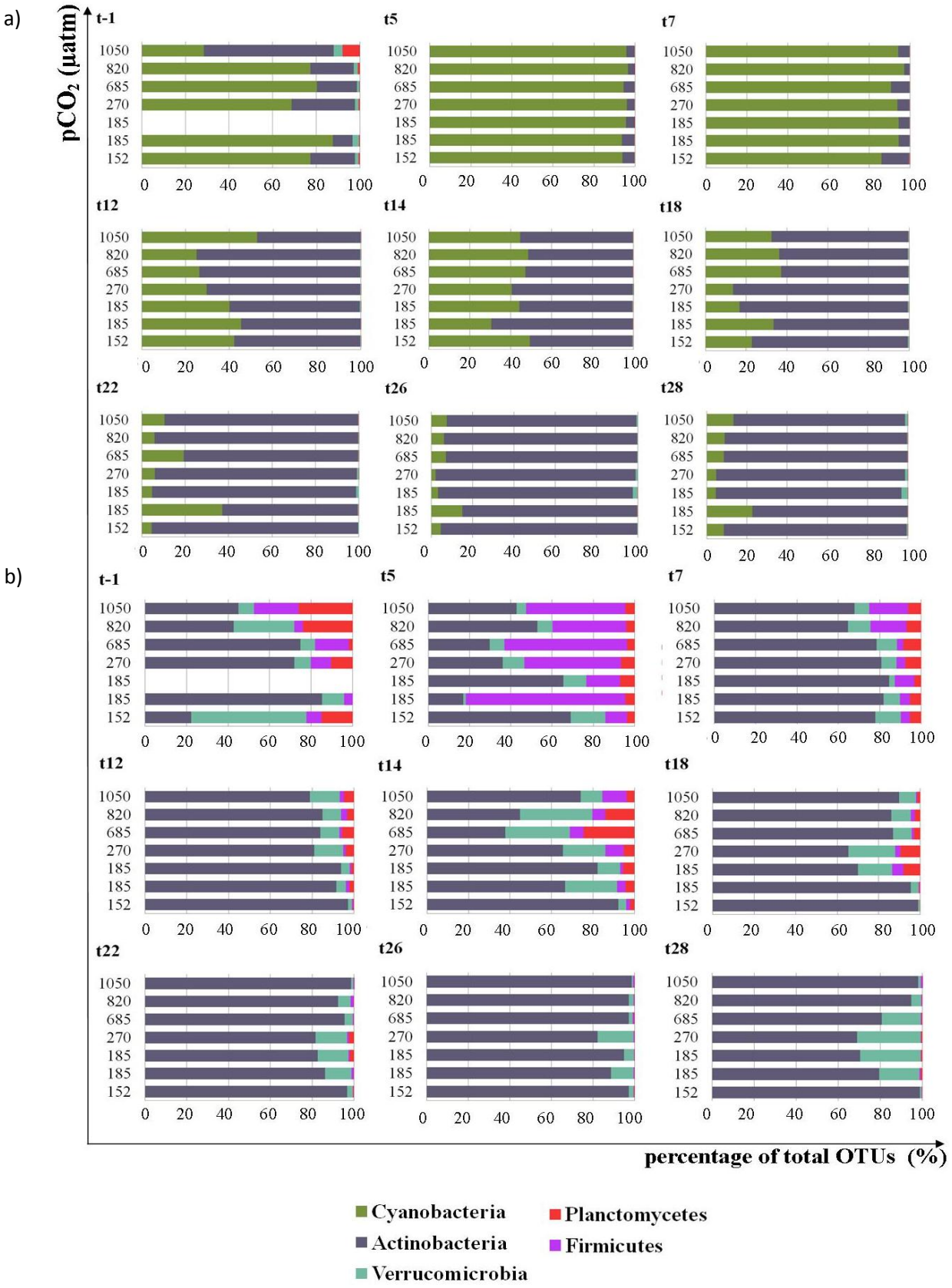

Fig. S2. Microbial community overview of the most abundant phyla classified as 'others' in Fig. 2 in **(a)** 'the free-living size fraction (0.2-3 µm) and **(b)** the particle-associated size fraction (3-20 µm) during t-1, t5, t7, t12, t14, t18, t22, t26 and t28; x-axis represents percentage of total OTUs and y-axis represents pCO_2 in µatm.

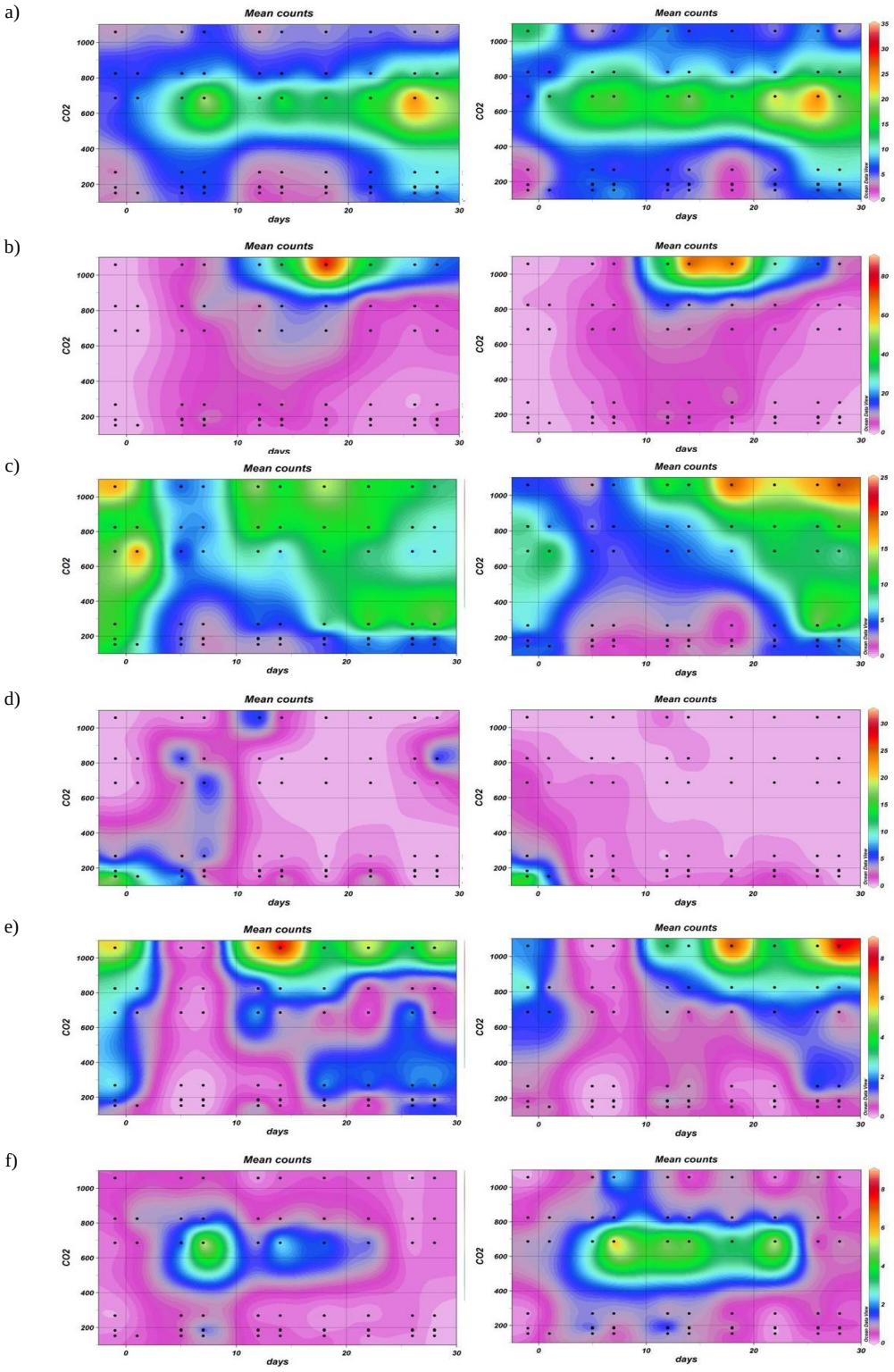

Fig. S3. Heat maps presenting the mean abundance count of **a)** Methylotenera (OTU # 114612) **b)** Oceanospirillaceae (OTU # 144699) **c)** Flavobacteriaceae (OTU # 151803) **d)** Leucothrix (OTU # 522744) **e)** Sphingobacteriales (OTU # 419525) **f)** Oxalobacteraceae (OTU # 94238) plotted against pCO_2 (µatm, y-axis) and time (days, x-axis). Left and right panel represent, respectively, the free living (0.2-3 µm) and particle-associated size fraction (3-20 µm).

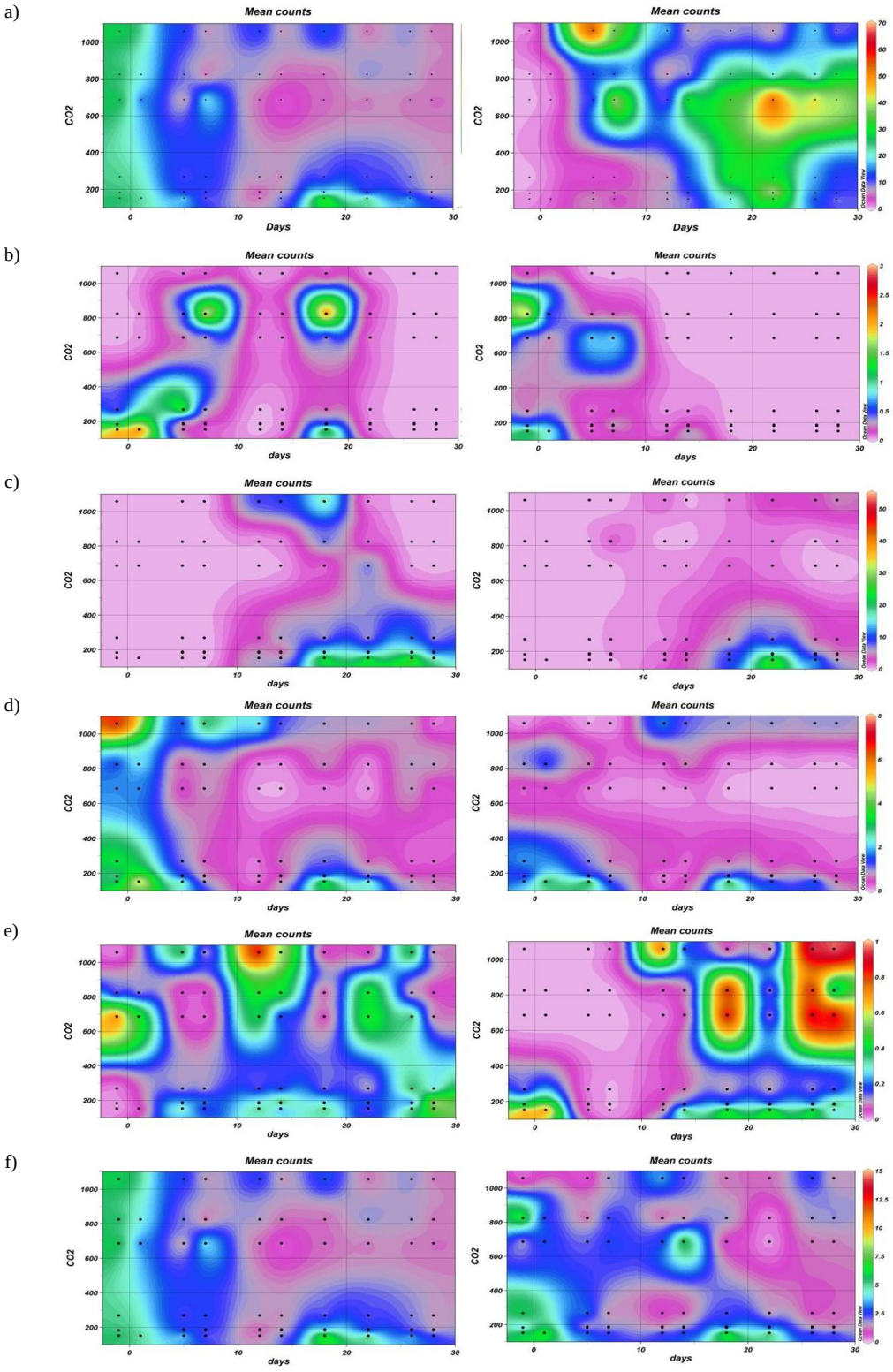

Fig. S4. Heat maps presenting the mean abundance count of **a)** Oleibacter (OTU # 592739) **b)** HTCC-2188 (OTU # 262549) **c)** Flavobacterium succinicians (OTU # 140859) **d)** Flavobacteria (OTU # 591187) **e)** Thioclava (OTU # 243032) **f)** SC3-41 (OTU # 554148) plotted against pCO_2 (µatm, y-axis) and time (days, x-axis). Left and right panel represent, respectively, the free living (0.2-3 µm) and particle-associated size fraction (3-20 µm).